

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2005, 04:35:15 ; Search time 1960 Seconds
(without alignments)
580.035 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20
Sequence: 1 gggacggcgctcggtcat 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1681110

Minimum DB seq length: 12
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 19 | 95.0 | 19 | 6 | CQ799992 Sequence |
| 4 | 16 | 80.0 | 21 | 6 | CQ799905 Sequence |
| 5 | 15 | 75.0 | 21 | 6 | CQ799906 Sequence |
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| 7 | 14.2 | 71.0 | 33 | 6 | AX473165 Sequence |
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| 9 | 13 | 65.0 | 20 | 6 | AR454276 Sequence |
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ALIGNMENTS

RESULT 1
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LOCUS CQ799984 20 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 82 from Patent WO2004030660.
ACCESSION CQ799984
VERSION CQ799984.1 GI:46848931

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Gleave,M.E., Rocchi,P. and Signaevsky,M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 82 15-APR-2004;
The University of British Columbia (CA)

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DEFINITION Sequence 81 from Patent WO2004030660.
ACCESSION CQ799983
VERSION CQ799983.1 GI:46848930
KEYWORDS Homo sapiens (human)
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Gleave, M.E., Rocchi, P. and Signaevsky, M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 81 15-APR-2004;
The University of British Columbia (CA)
LOCATION/Qualifiers

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DEFINITION Sequence 90 from Patent WO2004030660.
ACCESSION CQ799992
VERSION CQ799992.1 GI:46848939
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Gleave, M.E., Rocchi, P. and Signaevsky, M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 90 15-APR-2004;
The University of British Columbia (CA)
LOCATION/Qualifiers

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LOCUS CQ799905 21 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 3 from Patent WO2004030660.
ACCESSION CQ799905
VERSION CQ799905.1 GI:46848852
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Gleave, M.E., Rocchi, P. and Signaevsky, M.
TITLE Compositions for treatment of prostate and other cancers

JOURNAL Patent: WO 2004030660-A 3 15-APR-2004;
The University of British Columbia (CA)
LOCATION/Qualifiers

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DEFINITION Sequence 4 from Patent WO2004030660.
ACCESSION CQ799906
VERSION CQ799906.1 GI:46848853
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Gleave, M.E., Rocchi, P. and Signaevsky, M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 4 15-APR-2004;
The University of British Columbia (CA)
LOCATION/Qualifiers

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Qy 1 GGGACGGCGCTCG 15
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Db 7 GGGACGGCGCTCG 21
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LOCUS AR559501 33 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 16 from patent US 6750042.
ACCESSION AR559501
VERSION AR559501.1 GI:53968947
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Summers, A.O. and Cagliati, J.J.
TITLE Metal binding proteins, recombinant host cells and methods
JOURNAL Patent: US 6750042-A 16 15-JUN-2004;
University of Georgia Research Foundation, Inc.; Athens, GA
LOCATION/Qualifiers

FEATURES source
1. .33
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Db 6 GGGTCTCGGCGCTCGGCA 24

RESULT 7
AX473165
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DEFINITION Sequence 16 from Patent WO230962.
ACCESSION AX473165
VERSION AX473165.1 GI:22207875
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Summers,A.O. and Caguiat,J.J.
TITLE Metal binding proteins, recombinant host cells and methods
JOURNAL Patent: WO 0230962-A 16 18-APR-2002;
UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC. (US)

FEATURES
source
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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Best Local Similarity 84.2%; Pred. No. 2e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCA 19
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Db 6 GGGTCTCGGCGCTCGGCA 24

RESULT 8
E41696
LOCUS E41696 27 bp DNA linear PAT 31-JAN-2002
DEFINITION Process for producing L-glutamic acid by fermentation.
ACCESSION E41696
VERSION E41696.1 GI:18633367
KEYWORDS JP 2001069979-A/13.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 27)
AUTHORS Fujii,M. and Imanaka,T.
TITLE Process for producing L-glutamic acid by fermentation
JOURNAL Patent: JP 2001069979-A 13 21-MAR-2001;
JAPAN TOBACCO INC,TAKDAYUKI IMANAKA

COMMENT OS Artificial Sequence
PN JP 2001069979-A/13
PD 21-MAR-2001
PF 31-AUG-1999 JP 1999245121

PI MIKIO FUJII, TADAYUKI IMANAKA
PC C12N15/09,C12N1/21,C12P13/14,/(C12N1/21,C12R1:15), (C12P13/14,
C12R1:15),
PC C12N15/00
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QY 3 GACGCGCGCTCGGTCA 20
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Db 9 GACGCGCGAAGCCCAT 26

RESULT 9
AR454276
LOCUS AR454276 20 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 19 from patent US 6680425.
ACCESSION AR454276
VERSION AR454276.1 GI:42687423
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Rodriguez,R.L.
TITLE Chimeric plant promoters comprising sugar-regulatory sequences
JOURNAL Patent: US 6680425-A 19 20-JAN-2004;
The Regents of the University of California; Oakland, CA

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RESULT 10
BD243529
LOCUS BD243529/c 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Nucleotide fragment, probe, primer, reagent, and method for detecting nucleotide sequence derived from replication origin of pBR322.

ACCESSION BD243529
VERSION BD243529.1 GI:33053299
KEYWORDS JP 2002537856-A/36.
SOURCE unidentified
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 23)
AUTHORS Lamy,D.
TITLE Nucleotide fragment, probe, primer, reagent, and method for detecting nucleotide sequence derived from replication origin of pBR322.
JOURNAL Patent: JP 2002537856-A 36 12-NOV-2002;
TRANSGENE

COMMENT OS pBR322 plasmid
PN JP 2002537856-A/36
PD 12-NOV-2002
PF 03-MAR-2000 JP 2000603424
PR 05-MAR-1999 FR 99/02968
PI DIDIER LAMY
PC C12N15/09,C12Q1/68,C12N15/00
CC Nucleotide fragment, probe, primer, reagent, and method for
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CC nucleotide sequence derived from replication origin of pBR322
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FT Location/Qualifiers

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Db 16 CGTGCCTCGGTCGT 1

RESULT 11
AX034952/c
LOCUS AX034952 23 bp DNA linear PAT 15-NOV-2000
DEFINITION Sequence 36 from Patent WO0053803.
ACCESSION AX034952
VERSION AX034952.1 GI:11190877
KEYWORDS Cloning vector pBR322
SOURCE Cloning vector pBR322
ORGANISM Cloning vector pBR322
REFERENCE 1
AUTHORS Lamy D.
TITLE Nucleotide fragment, probe, primer, reagent and method for
detecting a nucleotide sequence derived from pBR322 replication
origin
JOURNAL Patent: WO 0053803-A 36 14-SEP-2000;
LAMY DIDIER (FR) ; TRANSGENE (FR)
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Db 16 CGTGCCTCGGTCGT 1

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AX684030
LOCUS AX684030 24 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 3 from Patent WO03006502.
ACCESSION AX684030
VERSION AX684030.1 GI:29371014
KEYWORDS Danio rerio (zebrafish)
SOURCE Danio rerio
ORGANISM Danio rerio
REFERENCE 1
AUTHORS Langheinrich U.
TITLE Isolation, characterization, and use of a teleost potassium channel
JOURNAL Patent: WO 03006502-A 3 23-JAN-2003;
Exelixis Deutschland GmbH (DE)
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Db 16 CGTGCCTCGGTCGT 1

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BD081436/c
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DEFINITION Production of proteins in plant seeds.
ACCESSION BD081436
VERSION BD081436.1 GI:22627039
KEYWORDS JP 2001518305-A/10.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Lemaux P.G., Cho M.J. and Buchanan R.B.
TITLE Production of proteins in plant seeds
JOURNAL Patent: JP 2001518305-A 10 16-OCT-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT OS Artificial sequence
PN JP 2001518305-A/10
PD 16-OCT-2001
PF 30-SEP-1998 JP 2000513959
PR 30-SEP-1997 US 60/060510
PI PEGGY G LEMAUX, MYEONG JE CHO, ROBERT B BUCHANAN PC
C12N15/09, A01H5/00, C12N5/10, C12N15/00, C12N5/00 CC Description of
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AR429358/c
LOCUS AR429358 24 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6642437.
ACCESSION AR429358
VERSION AR429358.1 GI:40189549
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Lemaux P.G., Cho M.-J. and Buchanan B.B.
TITLE Production of proteins in plant seeds
JOURNAL Patent: US 6642437-A 12 04-NOV-2003;
The Regents of the University of California; Oakland, CA
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Db 19 GCACGAGCGCTCGGATAT 1

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AR579704/c
LOCUS AR579704 24 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 14 from patent US 6784346.
ACCESSION AR579704
VERSION AR579704.1 GI:56583159

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
AUTHORS Cho, M.-J., Lemaux, P.G., Buchanan, B.B., Wong, J. and Marx, C.
TITLE Value-added traits in grain and seed transformed with thioredoxin
JOURNAL Patent: US 6784346-A 14 31-AUG-2004;
The Regents of the University of California; Oakland, CA

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Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 19 GCACGAGCGCTCGGATAT 1

Search completed: November 27, 2005, 05:29:43
Job time : 1963 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2005, 03:35:40 ; Search time 478 Seconds
(without alignments)
278.857 Million cell updates/sec

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Perfect score: 20
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Scoring table:
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Total number of hits satisfying chosen parameters: 4233410

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Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| c | 21 | 12.6 | 63.0 | 24 | 3 | AAC62482 | Aac62482 Wheat thi |
| c | 22 | 12.6 | 63.0 | 24 | 10 | AAD59639 | Aad59639 Bar ampli |
| c | 23 | 12.6 | 63.0 | 25 | 13 | ADS86174 | Ads86174 PCAV-deri |
| c | 24 | 12.6 | 63.0 | 29 | 4 | ABL96187 | AbL96187 Primer #3 |
| c | 25 | 12.6 | 63.0 | 30 | 2 | AAV44737 | Aav44737 Fluoresce |
| c | 26 | 12.6 | 63.0 | 31 | 2 | AAT38854 | Atc38854 Primer fo |
| c | 27 | 12.6 | 63.0 | 31 | 12 | ADO05568 | Ado05568 Plasmid R |
| c | 28 | 12.6 | 63.0 | 33 | 14 | AEA35882 | Aea35882 Mouse mid |
| c | 29 | 12.4 | 62.0 | 19 | 3 | AAA40594 | Aaa40594 Human Arp |
| c | 30 | 12.4 | 62.0 | 20 | 2 | AAQ36810 | Aaq36810 Oligomer |
| c | 31 | 12.4 | 62.0 | 20 | 2 | AAQ94968 | Aaq94968 PCR prime |
| c | 32 | 12.4 | 62.0 | 20 | 2 | AAV35805 | Aav35805 PCR prime |
| c | 33 | 12.4 | 62.0 | 20 | 2 | AAV99501 | Aav99501 Plasmid p |
| c | 34 | 12.4 | 62.0 | 20 | 8 | ADA16031 | Ada16031 Plasmid p |
| c | 35 | 12.4 | 62.0 | 20 | 9 | ACH03677 | Ach03677 Plasmid p |
| c | 36 | 12.4 | 62.0 | 20 | 10 | ADF73001 | Adf73001 Probe rel |
| c | 37 | 12.4 | 62.0 | 20 | 14 | ADW71639 | Adw71639 Plasmid p |
| c | 38 | 12.4 | 62.0 | 24 | 6 | ABQ07627 | Abq07627 Oligonuc |
| c | 39 | 12.4 | 62.0 | 24 | 6 | ABQ01856 | Abq01856 Oligonuc |
| c | 40 | 12.4 | 62.0 | 24 | 6 | ABQ07668 | Abq07668 Oligonuc |
| c | 41 | 12.4 | 62.0 | 24 | 12 | ADO38198 | Ado38198 HIV envel |
| c | 42 | 12.4 | 62.0 | 24 | 12 | ADO38213 | Ado38213 HIV envel |
| c | 43 | 12.4 | 62.0 | 24 | 12 | ADO38185 | Ado38185 HIV envel |
| c | 44 | 12.4 | 62.0 | 24 | 12 | ADO38102 | Ado38102 HIV envel |
| c | 45 | 12.4 | 62.0 | 24 | 12 | ADO38074 | Ado38074 HIV envel |

ALIGNMENTS

RESULT 1
ADM94732
ID ADM94732 standard; DNA; 20 BP.

XX ADM94732;

XX 01-JUL-2004 (first entry)

DE Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:82.

DE heat shock protein 27; hsp27; cytostatic; gene therapy;

KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;

KW antisense oligonucleotide; ss.

XX Homo sapiens.

OS Synthetic.

XX WO2004030660-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WO-CA001588.

XX 02-OCT-2002; 2002US-0415859P.

PR 18-APR-2003; 2003US-0463952P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave MB, Rocchi P, Signaevsky M;

XX WPI; 2004-316331/29.

PT New composition comprising a therapeutic agent that reduces the amount of active hsp27 in hsp27 expressing cells exposed to the therapeutic agent, useful in treating cancer, e.g., prostate cancer or a central nervous system malignancy.

XX Claim 6; SEQ ID NO 82; 38pp; English.

CC The present invention describes a composition which comprises a

CC therapeutic agent that reduces the amount of active heat shock protein 27

CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The

DE Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:3.
XX
KW heat shock protein 27; hsp27; cytostatic; gene therapy;
KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW antisense oligonucleotide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO2004030660-A2.
XX
XX 15-APR-2004.
XX
XX 02-OCT-2003; 2003WO-CA001588.
XX
XX 02-OCT-2002; 2002US-0415859P.
XX
XX 18-APR-2003; 2003US-0463952P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Gleave ME, Rocchi P, Signaevsky M;
XX WPI; 2004-316331/29.
XX
XX New composition comprising a therapeutic agent that reduces the amount of
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT useful in treating cancer, e.g., prostate cancer or a central nervous
PT system malignancy.
XX
XX Claim 5; SEQ ID NO 3; 38pp; English.
XX
XX The present invention describes a composition which comprises a
CC therapeutic agent that reduces the amount of active heat shock protein 27
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC composition has cytostatic activity, and can be used in gene therapy. The
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC cancer or a central nervous system malignancy. The present sequence
CC represents a human hsp27 antisense oligonucleotide which is used in the
CC exemplification of the present invention.
XX
XX Sequence 21 BP; 1 A; 7 C; 9 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 80.0%; Score 16; DB 12; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 8.2e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 5 CGCGGCGCTCGGTCAT 20
Db 1 CGCGGCGCTCGGTCAT 16
XX
RESULT 5
ADM94654
ID ADM94654 standard; DNA; 21 BP.
XX
XX ADM94654;
XX
XX AC
XX
XX 01-JUL-2004 (first entry)
XX
XX Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:4.
DE
XX
XX heat shock protein 27; hsp27; cytostatic; gene therapy;
KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW antisense oligonucleotide; ss.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO2004030660-A2.
XX
XX 15-APR-2004.
XX

PF 02-OCT-2003; 2003WO-CA001588.
XX
XX 02-OCT-2002; 2002US-0415859P.
XX
XX 18-APR-2003; 2003US-0463952P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA
XX Gleave ME, Rocchi P, Signaevsky M;
PI WPI; 2004-316331/29.
XX
XX New composition comprising a therapeutic agent that reduces the amount of
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT useful in treating cancer, e.g., prostate cancer or a central nervous
PT system malignancy.
XX
XX Claim 5; SEQ ID NO 4; 38pp; English.
XX
XX The present invention describes a composition which comprises a
CC therapeutic agent that reduces the amount of active heat shock protein 27
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC composition has cytostatic activity, and can be used in gene therapy. The
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC cancer or a central nervous system malignancy. The present sequence
CC represents a human hsp27 antisense oligonucleotide which is used in the
CC exemplification of the present invention.
XX
XX Sequence 21 BP; 4 A; 5 C; 11 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 75.0%; Score 15; DB 12; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 2.4e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GGGACGCGCGGCTCG 15
Db 7 GGGACGCGCGGCTCG 21
XX
RESULT 6
ABK52211
ID ABK52211 standard; DNA; 33 BP.
XX
XX ABK52211;
XX
XX 13-AUG-2002 (first entry)
XX
XX Synthetic product 2 reverse PCR primer for construction of pASK-MBD.
DE
XX
XX Mercuric ion; contaminated soil; ground water; hydroponic solution;
KW irrigation water; waste stream; contaminated aqueous medium;
KW biological fluid; gastrointestinal tract; chelon protein;
KW enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
KW heavy metal binding protein; pASK-MBD; PCR; primer; ss.
XX
XX Synthetic.
OS
XX WO200230962-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001WO-US031819.
PF
XX
XX 12-OCT-2000; 2000US-0240465P.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
PA
XX Summers AO, Caguiat JJ;
PI WPI; 2002-435437/46.
XX
XX Novel non-naturally occurring recombinant DNA molecule encoding a chelon
PT protein useful for binding divalent cation mercury from contaminated
PT

PT soil, water, aqueous medium including biological fluids.
 XX Disclosure; Page 24; 42pp; English.
 XX
 CC The present invention relates to a new non-naturally occurring
 CC recombinant DNA molecule comprising a sequence encoding a chelon protein
 CC which binds mercuric ions. The invention is useful for recombinantly
 CC producing a protein in a host-cell, by infecting or transforming a host
 CC cell capable of expressing a chelon coding sequence with a vector
 CC comprising a promoter active in the host cell operably linked to a coding
 CC region for the protein to produce a recombinant host cell and culturing
 CC the recombinant host cell under conditions, where DNA is expressed. The
 CC nucleic acid encoding the chelon protein is useful for binding divalent
 CC mercuric ions, to take up, sequester and concentrate the heavy metal ions
 CC from contaminated soil, ground water, hydroponic solutions or irrigation
 CC water of waste streams. The DNA of the invention, when immobilised onto a
 CC solid support, is useful for concentrating heavy metal ions from
 CC contaminated environment waste streams or contaminated aqueous medium
 CC including biological fluids. The nucleic acid, when recombinantly
 CC expressed in enteric bacteria (which are nontoxic and nonpathogenic),
 CC is suitable for use in the in vivo sequestration and elimination of
 CC mercuric ion from gastrointestinal tracts of animals or humans exposed to
 CC toxic metal ions such as mercury and/or cadmium. The molecules of the
 CC invention are also useful in water treatment resins. The nucleic acid of
 CC the invention is highly specific and binds divalent cation such as
 CC mercury or cadmium with high affinity. The present nucleic acid sequence
 CC represents synthetic product 2 reverse PCR primer that was used in the
 CC methods of the invention for construction of pASK-MBD vector
 XX
 SQ Sequence 33 BP; 6 A; 8 C; 12 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 6; Length 33;
 Best Local Similarity 84.2%; Pred. No. 5.4e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGCGCTCGGTCA 19
 ||| |||||
 Db 6 GGGTCTCGCGCTCGGGCA 24

RESULT 7
 ACH58106
 ID ACH58106 standard; DNA; 25 BP.
 XX
 AC ACH58106;
 XX
 DT 16-OCT-2003 (first entry)
 XX
 DE DNA target sequence #7242 useful in array for genetic analyses.
 XX
 KW Gene expression analysis; array; hybridisation; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridisation;
 KW library screening; Southern hybridisation; northern hybridisation;
 KW dot-blot hybridisation; gene sequence; mutation detection;
 KW target sequence; probe; PCR; primer; ss.

OS Unidentified.
 XX
 XX US2003082596-A1.
 PN
 XX
 XX 01-MAY-2003.
 PD
 XX
 XX 08-AUG-2002; 2002US-00215112.
 PF
 XX
 XX 08-AUG-2001; 2001US-0311040P.
 PR
 XX
 XX (MITT/) MITTMANN M.
 PA
 XX
 XX Mittmann M;
 PI
 XX
 XX WPI; 2003-576608/54.
 DR
 XX
 XX New probe array useful e.g. for monitoring gene expression levels, for

PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
 PT comprises multiple nucleic acid probes.
 XX
 PS Claim 1; SEQ ID NO 7242; 9pp; English.
 XX

CC The present invention relates to nucleic acid sequences that are
 CC complementary to particular genes, and can be used as probes for a
 CC variety of analyses such as gene expression analysis. Each probe
 CC comprises 9 or more consecutive nucleotides from at least one of 14936
 CC nucleotide sequences defined in the patent, or their perfect sense match,
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
 CC The probes may be used in an array comprising at least 10 distinct
 CC nucleic acid probes. The array is useful in monitoring gene expression
 CC levels by hybridisation to a DNA library, in analysing genetic
 CC variations, and in hybridising tag-labelled compounds. The probes are
 CC useful for identifying family members of a gene. The probes are also
 CC useful in situ hybridisations, in screening cDNA or genomic libraries
 CC (or derived subclones) for additional clones containing segments of DNA
 CC that have been previously isolated and sequenced, in Southern, northern,
 CC or dot-blot hybridisation of genomic DNA to identify or detect the
 CC sequence of any gene or detect specific mutations in any gene, and in
 CC mapping the 5' termini of mRNA molecules by primer extensions. The
 CC nucleic acid sequences of the invention are also useful as PCR primers.
 CC The invention provides a large collection of nucleic acid sequences
 CC complementary to particular genes with a wide range of analytical uses.
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
 CC The sequence data for this patent was obtained in electronic format
 CC directly from the USPTO web site at seqdata.uspto.gov/psipdIDentry.html
 XX

SQ Sequence 25 BP; 4 A; 9 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACGGCGCGCTCG 15
 |||||
 Db 2 GGACGGCGCGCTCG 15

RESULT 8
 AC103862/c
 ID AC103862 standard; DNA; 25 BP.
 XX
 AC AC103862;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 3853.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 XX US2003104410-A1.
 PN
 XX
 XX 05-JUN-2003.
 PD
 XX
 XX 15-MAR-2002; 2002US-00098263.
 PF
 XX
 XX 16-MAR-2001; 2001US-0276759P.
 PR
 XX
 XX (AFFY-) AFFYMETRIX INC.
 PA
 XX
 XX Mittmann MP;
 PI
 XX
 XX WPI; 2003-567953/53.
 DR
 XX
 XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 3853; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. CC Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, CC in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis CC of at least one target sequence. The method of analysis comprises CC hybridising at least one or more nucleic acids to at least two or more CC nucleic acid probes and detecting the hybridisation. The nucleic acid CC probes are attached to a solid support. The analysis comprises monitoring CC gene expression levels, identifying biallelic markers or polymorphisms, CC or family members of a gene and a cross-species comparison. Each of the CC nucleic acids further comprises a tag sequence. The array of nucleic acid CC probes is useful in situ hybridisation, in Southern, Northern or dot- CC blot hybridisation to identify or detect the sequence or specific CC mutations of any gene, in mapping the 5' termini of mRNA molecules by CC primer extensions or in screening cDNA or genomic libraries or subclones CC for additional subclones containing segments of DNA that have been CC isolated and previously sequenced. The sequence presented is one of the CC nucleic acid probes incorporated in the microarray. Note: The sequence CC data for this patent can also be obtained in electronic format directly CC from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 6 A; 8 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGACGGCGCGCTCGGTCA 19
||||| ||||| ||||| ||||| |||||

Db 24 GGACTCGTCGTCGTCA 7

RESULT 9

AC165798

ID AC165798 standard; DNA; 25 BP.

XX AC AC165798;

XX 14-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 65789.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 65789; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. CC Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, CC in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis CC of at least one target sequence. The method of analysis comprises CC hybridising at least one or more nucleic acids to at least two or more CC nucleic acid probes and detecting the hybridisation. The nucleic acid CC probes are attached to a solid support. The analysis comprises monitoring CC gene expression levels, identifying biallelic markers or polymorphisms, CC or family members of a gene and a cross-species comparison. Each of the CC nucleic acids further comprises a tag sequence. The array of nucleic acid CC probes is useful in situ hybridisation, in Southern, Northern or dot- CC blot hybridisation to identify or detect the sequence or specific CC mutations of any gene, in mapping the 5' termini of mRNA molecules by CC primer extensions or in screening cDNA or genomic libraries or subclones CC for additional subclones containing segments of DNA that have been CC isolated and previously sequenced. The sequence presented is one of the CC nucleic acid probes incorporated in the microarray. Note: The sequence CC data for this patent can also be obtained in electronic format directly CC from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 4 A; 8 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GACGGCGCGCTCGGTCA 20
||||| ||||| ||||| ||||| |||||

Db 5 GACCGGAGCTCGGTGCT 22

RESULT 10

AAH21740

ID AAH21740 standard; DNA; 27 BP.

XX AC AAH21740;

XX 14-AUG-2001 (first entry)

DE Corynebacterium glutamicum chaperone CpkB related PCR primer SEQ:13.

XX Corynebacterium glutamicum; chaperone; chaperonin; CpkB; groEL;
KW fermentation; L-glutamic acid; thermophilic microbe; PCR primer; ss.

XX Corynebacterium glutamicum.

XX JP2001069979-A.

XX 21-MAR-2001.

XX 31-AUG-1999; 99JP-00245121.

XX 31-AUG-1999; 99JP-00245121.

XX (NIBS) JAPAN TOBACCO INC.

XX (BEAB-) BE ABLE KK.

XX WPI; 2001-321175/34.

XX Preparation of L-glutamic acid by fermentation.

XX Example 1; Page 11; 18pp; Japanese.

XX The present invention describes an L-glutamic acid-producing microbe (I) CC or its mutant which expresses the molecular chaperone derived from a CC thermophilic microbe and produces stably L-glutamic acid at a temperature CC near the upper limit of optimum growth or higher. (I) or its mutant CC transformed by a recombinant DNA containing a gene encoding the molecular

CC chaperone derived from a thermophilic microbe and a promoter operably
 CC associated with a gene (II) comprising: (a) a fully defined 1661 base
 CC pair (bp) sequence (AAH21757); (b) a nucleic acid sequence encoding a
 CC protein comprising: (i) a base sequence in which 1-20 bases are deleted,
 CC replaced or added in AAH21757; or (ii) at least one base is deleted,
 CC or replaced or added in a fully defined 519 base sequence (AAH21768), and
 CC having molecular chaperone activity in (I). Also described is a method
 CC for the preparation of L-glutamic acid by fermentation in which the
 CC transformed (I) is used and cultured at a high temperature limiting the
 CC production of L-glutamic acid with the untransformed (I). The microbe can
 CC be used for the preparation of L-glutamic acid. The present sequence
 CC represents a PCR primer used in the preparation of *Corynebacterium*
 CC glutamicum chaperone CpkB, which is used in an example from the present
 CC invention
 XX
 SQ Sequence 27 BP; 4 A; 9 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 4; Length 27;
 Best Local Similarity 83.3%; Pred. No. 1.6e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GACGCGCGCTCGTCAT 20
 Db ||||| ||||| ||||| |||||

9 GACGCGCGCAACGCCAT 26

RESULT 11
 AAV51704/c
 ID AAV51704 standard; DNA; 21 BP.
 XX
 AC AAV51704;
 XX
 DT 02-FEB-1999 (first entry)
 XX
 DE Zea mays genome forward PCR primer #304.
 XX
 KW Polymorphic marker; allele-specific; probe; amplification; PCR primer;
 KW hybridisation; plant; hybrid certification; genetic contribution;
 KW progeny; back-cross; hybrid; ancestry; corn; ss.
 XX
 OS Synthetic.
 OS Zea mays.
 XX
 FN WO9824796-A1.
 XX
 PD 11-JUN-1998.
 XX
 PF 01-DEC-1997; 97WO-US021782.
 XX
 PR 02-DEC-1996; 96US-0032069P.
 PR 07-MAR-1997; 97US-00813507.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Lemieux B, Landry BS, Sapolsky RJ, Murigneux A;
 XX
 DR WPI; 1998-333252/29.
 XX
 FT Brassica species allele-specific oligonucleotide probes and primers -
 FT useful for plant breeding.
 XX
 PS Example 1; Page 55; 65pp; English.
 XX
 CC AAV51401-V51704 are forward PCR primers used to amplify fragments of the
 CC Zea mays genome in order to detect polymorphic markers. Such markers can
 CC be used in the construction of allele-specific primers and probes for
 CC amplification or hybridisation, e.g. to determine common or disparate
 CC ancestry between 2 or more plants, to monitor the genetic contribution of
 CC an ancestral plant, to trace the progeny of proprietary plants, in
 CC certification of a hybrid plant or to identify the progeny of a back-
 CC crossed plant with an ancestral plant
 XX
 SQ Sequence 21 BP; 3 A; 11 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 2; Length 21;
 Best Local Similarity 87.5%; Pred. No. 2.4e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGG 16
 Db ||||| ||||| ||||| |||||

16 GGGACGCGCGCTCGG 1

RESULT 12
 AAA75395/c
 ID AAA75395 standard; DNA; 23 BP.
 XX
 AC AAA75395;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE Fragment derived from the origin of replication of pBR322.
 XX
 KW pBR322 plasmid; probe; primer; origin of replication;
 KW Gene therapy vector; ss.
 XX
 OS Synthetic.
 OS
 PN WO200053803-A1.
 XX
 PD 14-SEP-2000.
 XX
 PF 03-MAR-2000; 2000WO-FR000543.
 XX
 PR 05-MAR-1999; 99FR-00002968.
 XX
 PA (TRGE) TRANSGENE.
 XX
 PI Lamy D;
 XX
 DR WPI; 2000-587445/55.
 XX
 PT Nucleic acid sequences that hybridize to the pBR322 origin of
 PT replication, useful for monitoring gene therapy vectors, and as probes or
 PT primers.
 XX
 PS Claim 3; Page 26; 36pp; French.
 XX
 CC AAA75311-41 and AAA75393-A75402 are derived from the origin of
 CC replication of the pBR322 plasmid. The nucleic acid fragments are useful
 CC as probes and primers for detecting sequences derived from the origin of
 CC replication of pBR322 or vectors (or their fragments) that contain such
 CC sequences. They are particularly used to monitor the presence of gene
 CC therapy vectors (used to deliver therapeutic genes or proteins, antisense
 CC sequences or ribozymes), e.g. for determining disappearance of the
 CC vector, for adjustment of treatment, or for timing of new treatments.
 CC They can also be used to screen foods and cosmetics for the presence of
 CC derived materials from genetically modified organisms
 XX
 SQ Sequence 23 BP; 6 A; 7 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 3; Length 23;
 Best Local Similarity 87.5%; Pred. No. 2.4e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGCGCGCGCTCGTCAT 20
 Db ||||| ||||| ||||| |||||

16 CGCTGCGCTCGGTCGT 1

RESULT 13
 ABZ58873
 ID ABZ58873 standard; DNA; 24 BP.
 XX
 AC ABZ58873;
 XX

DT 27-OCT-2003 (revised)
DT 28-APR-2003 (first entry)
XX
DE Zebrafish ZERG mRNA inhibiting antisense oligonucleotide.
XX
KW Teleost; zebrafish; ZERG; cardiovascular; antiarrhythmic; cytostatic;
KW neuroprotective; gene therapy; potassium channel; antisense; ss.
XX
OS Danio rerio.
XX
XX WO2003006502-A2.
XX
XX 23-JAN-2003.
XX
XX 11-JUL-2002; 2002WO-IB004280.
XX
XX 13-JUL-2001; 2001US-0305396P.
XX
XX (ARTE-) ARTEMIS PHARM GMBH.
XX
XX Langheintich U;
XX
XX WPI; 2003-210421/20.
XX
XX New teleost (specifically zebrafish) ERG genes, which encode ERG family
PT potassium channels, useful for studying e.g. cardiac or brain function,
PT or for developing treatments for e.g. cardiac diseases, cancer or
PT neurological diseases.
XX
XX Claim 7; Page 28; 55pp; English.
XX
XX The invention relates to a teleost (zebrafish) ERG (ZERG) polypeptide.
CC The ZERG nucleic acid molecule is useful for studying cardiac function,
CC abnormal heart beat phenotype, or long QT syndrome (an abnormality of
CC cardiac muscle repolarization that predisposes affected individuals to
CC lethal arrhythmias). The zebrafish comprising ZERG gene is useful as
CC models for cardiac function or disease. The ZERG genes are particularly
CC useful for in (non-)cardiac researches, or for developing treatments for
CC cardiac diseases, tumours or cancers, brain and nervous system disorders
CC or neurological diseases, or insulin-related diseases. The present
CC sequence represents the zebrafish ZERG mRNA inhibiting antisense
CC oligonucleotide. (Updated on 27-OCT-2003 to standardise OS field)
XX
SQ Sequence 24 BP; 4 A; 8 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 8; Length 24;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGCGCGCGCTCGGTCA 20
DB 9 CGCGCGCGCACGGCAT 24

RESULT 14
ACI84537/C
ID ACI84537 standard; DNA; 25 BP.
XX
XX ACI84537;
AC
XX 14-OCT-2003 (first entry)
DT
DE Human microarray DNA oligonucleotide SEQ ID NO 84528.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
OS
XX US2003104410-A1.
PN
XX 05-JUN-2003.
PD

XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Mittmann MP;
PI
XX WPI; 2003-567953/53.
DR
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 84528; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 4 A; 9 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGACCGCGCGCTCGG 16
DB 16 GGGACACGGCACTCGG 1

RESULT 15
ADO31537
ID ADO31537 standard; DNA; 29 BP.
XX
XX ADO31537;
AC
XX 26-AUG-2004 (first entry)
DT
DE Human CFTR gene wild-type probe for variant S549N.
XX
XX Human; CFTR gene; ss; probe; cystic fibrosis;
KW Cystic Fibrosis Transmembrane Conductance Regulator;
KW invasive cleavage structure assay; INVADER; PRET;
KW fluorescent resonance energy transfer; multiplexed amplification.
XX
XX Homo sapiens.
OS
XX WO2004046688-A2.
PN
XX 03-JUN-2004.
PD

PF 14-NOV-2003; 2003MO-US036611.
XX
PR 14-NOV-2002; 2002US-0426144P.
PR 21-FEB-2003; 2003US-00371913.
PR 26-JUN-2003; 2003US-00608577.
PR 21-JUL-2003; 2003US-0489095P.
PR 25-AUG-2003; 2003US-0497644P.
PR 28-OCT-2003; 2003US-0515175P.
PR 14-NOV-2003; 2003US-00713653.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Accola M, Wigdal SS, Mast AL, Bartholomay CT, Kwiatkowski RW;
PI Tevere V, Ip HS, Carroll K, Peterson P, Agarwal P, Jarvis N;
PI Hall JG, Heisler L;
XX
DR WPI; 2004-420702/39.
XX
PT Detecting Cystic Fibrosis Transmembrane Conductance Regulator (CFTR)
PT alleles, useful for screening mutations associated with cystic fibrosis,
PT comprises exposing amplified CFTR target nucleic acid to detection
PT assays.
XX
XX Example 7; SEQ ID NO 169; 147pp; English.
XX
CC The invention relates to detecting Cystic Fibrosis Transmembrane
CC Conductance Regulator (CFTR) alleles comprising providing a sample
CC comprising a CFTR target nucleic acid, amplifying the CFTR target nucleic
CC acid with 25 cycles or fewer of a PCR to generate amplified target
CC nucleic acid, and exposing the amplified target nucleic acid to detection
CC assays configured to detect CFTR alleles under conditions such that the
CC presence or absence of the CFTR alleles is detected, using an invasive
CC cleavage structure assay (designated INVADER), employing FRET probes
CC (fluorescent resonance energy transfer). Also included is a kit
CC comprising a non-amplified oligonucleotide detection assay configured for
CC detecting at least one CFTR allele or oligonucleotide detection assays
CC configured for detecting a set of CFTR alleles where the set is a first
CC set comprising 2789+5G to A, R1162X, R560T, 1898+1 G to A, del1507,
CC 1148T, and A455E, a second set comprising 3120+1G to A, 3659delC, G551D,
CC N1303K, 1078delT, R334W, 711+1G to T, and 3849+10kb, a third set
CC comprising 621+1G to T, W1282X, 1717-1G to A, and R117H, or a fourth set
CC comprising R347P, G85E, G542X and R553X, or a fifth set comprising
CC 2184delA. The non-amplified oligonucleotide detection assay or the
CC oligonucleotide detection assays comprises first and second
CC oligonucleotides configured to form an invasive cleavage structure in
CC combination with a target sequence comprising the CFTR allele. The first
CC oligonucleotide comprises a 5' portion and a 3' portion, where the 3'
CC portion is configured to hybridise to the target sequence and the 5'
CC portion is configured to not hybridise to the target sequence. The second
CC oligonucleotide comprises a 5' portion and a 3' portion, where the 5'
CC portion is configured to hybridise to the target sequence and the 3'
CC portion is configured to not hybridise to the target sequence. The method
CC and kit are useful for detecting CFTR alleles, more particularly for
CC screening nucleic acid samples e.g. from patients, for the presence of
CC any one of a collection of mutations in the CFTR gene associated with
CC cystic fibrosis. The method and compositions are useful for generating
CC and analysing limited cycle, multiplexed amplification of a large
CC collection of CFTR loci. The present sequence comprises a probe for the
CC method of the invention detecting the wild-type CFTR allele.
XX
SQ Sequence 29 BP; 6 A; 9 C; 9 G; 5 T; 0 U; 0 Other;
Query Match 64.0%; Score 12.8; DB 12; Length 29;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GGACGGCGGCTCGGT 17
Db |||||
3 GGACGGGAGCTCAGT 18

Search completed: November 27, 2005, 04:56:51
Job time : 481 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 27, 2005, 04:44:55 ; Search time 3610 Seconds
(without alignments)
259.208 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20
Sequence: 1 gggacgcgcgtcgatc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 76294

Minimum DB seq length: 12
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| C 1 | 12.8 | 64.0 | 32 | 2 | BF131807 |
| C 2 | 12.4 | 62.0 | 26 | 10 | AG203073 |
| C 3 | 12.2 | 61.0 | 28 | 1 | AI287864 |
| C 4 | 12 | 60.0 | 31 | 1 | AA867755 |
| C 5 | 12 | 60.0 | 31 | 10 | CZ169504 |
| C 6 | 11.4 | 57.0 | 31 | 9 | AZ826864 |
| C 7 | 11.2 | 56.0 | 23 | 10 | AJ587908 |
| C 8 | 11.2 | 56.0 | 31 | 6 | CD028820 |
| C 9 | 11 | 55.0 | 21 | 9 | AZ420773 |
| C 10 | 11 | 55.0 | 33 | 10 | AJ599957 |
| C 11 | 11 | 55.0 | 34 | 1 | AA259780 |
| C 12 | 10.6 | 53.0 | 25 | 1 | AI758887 |
| C 13 | 10.6 | 53.0 | 25 | 6 | CF643223 |
| C 14 | 10.6 | 53.0 | 25 | 6 | CF643257 |
| C 15 | 10.6 | 53.0 | 33 | 10 | AG216212 |
| C 16 | 10.6 | 53.0 | 35 | 6 | CF298077 |
| C 17 | 10.6 | 53.0 | 35 | 6 | CF642505 |
| C 18 | 10.6 | 53.0 | 35 | 8 | DR108402 |
| C 19 | 10.4 | 52.0 | 22 | 3 | BM398778 |
| C 20 | 10.4 | 52.0 | 26 | 10 | CG731752 |
| C 21 | 10.4 | 52.0 | 27 | 11 | TA103C01P |
| C 22 | 10.4 | 52.0 | 28 | 1 | AI256473 |

| | | | | | |
|------|------|------|----|----|-----------|
| C 23 | 10.4 | 52.0 | 29 | 9 | CC456807 |
| C 24 | 10.4 | 52.0 | 31 | 10 | CG724391 |
| C 25 | 10.4 | 52.0 | 34 | 8 | N55046 |
| C 26 | 10.4 | 52.0 | 34 | 9 | AZ346691 |
| C 27 | 10.2 | 51.0 | 25 | 1 | AI002379 |
| C 28 | 10.2 | 51.0 | 27 | 6 | CF277108 |
| C 29 | 10.2 | 51.0 | 28 | 1 | AB080287 |
| C 30 | 10.2 | 51.0 | 28 | 1 | AI358659 |
| C 31 | 10.2 | 51.0 | 29 | 1 | AW246529 |
| C 32 | 10.2 | 51.0 | 30 | 1 | AJ746806 |
| C 33 | 10.2 | 51.0 | 30 | 10 | CZ472135 |
| C 34 | 10.2 | 51.0 | 31 | 1 | AA912813 |
| C 35 | 10.2 | 51.0 | 31 | 3 | BI915569 |
| C 36 | 10.2 | 51.0 | 33 | 10 | AJ600534 |
| C 37 | 10.2 | 51.0 | 33 | 11 | DME545177 |
| C 38 | 10.2 | 51.0 | 34 | 1 | AA737625 |
| C 39 | 10.2 | 51.0 | 34 | 10 | CG712020 |
| C 40 | 10 | 50.0 | 21 | 9 | AZ513847 |
| C 41 | 10 | 50.0 | 22 | 8 | DR103042 |
| C 42 | 10 | 50.0 | 27 | 9 | AZ769255 |
| C 43 | 10 | 50.0 | 30 | 1 | AJ746842 |
| C 44 | 10 | 50.0 | 30 | 10 | CZ472687 |
| C 45 | 10 | 50.0 | 30 | 10 | CZ488898 |

ALIGNMENTS

RESULT 1
BF131807/c
LOCUS 601820724F1 NTH_MGC_58 Homo sapiens cDNA clone IMAGE:4052596 5', mRNA linear EST 24-OCT-2000
DEFINITION mRNA sequence.
ACCESSION BF131807.1 GI:10970847
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 32)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: L1CM889 row: p column: 05
High quality sequence start: 8
High quality sequence stop: 30.
FEATURES
Location/Qualifiers
1..32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4052596"
/tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_58"
/note="Organ: Kidney; Vector: pNR-LIB (Clontech); Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggcgctcgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGAGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average

insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 64.0%; Score 12.8; DB 2; Length 32;
Best Local Similarity 87.5%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGCGCGCTCGGTCAT 20
|||||
Db 27 CGCTGCGCTCGGTCGT 12

RESULT 2
AG203073
LOCUS
DEFINITION Pan troglodytes DNA, clone: RP43-087B01.T7, genomic survey
sequence.

ACCESSION AG203073
VERSION AG203073.1 GI:45235248
KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.

REFERENCE 1
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.

TITLE BAC end sequences of Library RP-43
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 26)
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.

TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)

COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI.

Location/Qualifiers

1. .26
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-087B01.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 62.0%; Score 12.4; DB 10; Length 26;
Best Local Similarity 92.9%; Pred. No. 3.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTC 14
|||||
Db 1 GGGACTCGGCGCTC 14

RESULT 3
AI287864/c

LOCUS AI287864 28 bp mRNA linear EST 24-NOV-1998
DEFINITION QV07d12.x1 NCI CGAP Kid8 Homo sapiens cDNA clone IMAGE:1980887 3',
similar to SW-CA44 HUMAN P33420 COLLAGEN ALPHA 4(IV) CHAIN
PRECURSOR. ; contains MER22.B3 TAR1 repetitive element ;, mRNA
sequence.

ACCESSION AI287864
VERSION AI287864.1 GI:3927617
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 28)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .28

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1980887"

/issue_type="renal cell tumor"

/lab_host="DH10B"

/clone_lib="NCI-CGAP Kid8"

/notes="Organ: Kidney; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.2 kb. Life Technologies catalog #:

11524-014"

ORIGIN

Query Match 61.0%; Score 12.2; DB 1; Length 28;
Best Local Similarity 82.4%; Pred. No. 4.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGT 17
|||||
Db 21 GGGCGGGCGGCGCGGT 5

RESULT 4

AA867755/c

LOCUS

DEFINITION vx16b08.r1 Soares thymus 2NDMT Mus musculus cDNA clone
IMAGE:1264599 5', similar to TR:O35394 O35394 PRENYLATED RAB
ACCEPTOR 1. ;, mRNA sequence.

ACCESSION AA867755

VERSION AA867755.1 GI:2963200

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 31)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Contact: GATC
German Genetrapp Consortium (GGTC)
Email: info@genetrapp.de
U3CEO gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
'http://genetrapp.gsf.de/project/web_new/database/result_clone.html?
clone_id=G050C04'. ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrapp.gsf.de/project/web_new/order_clones/howtoorder.htm#
1'. Inhouse Sequence Identifier: 16629
Class: Gene Trap.

FEATURES
source
1..31
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="G050C04"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells (C57BL/6J x 129Sv/SvEvTac) F1"
/clone_lib="GGTC Gene Trap Library GV07C05"
/note="Vector: U3CEO"

ORIGIN
Query Match 60.0%; Score 12; DB 10; Length 31;
Best Local Similarity 75.0%; Pred. No. 5.7e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCAAT 20
||||| ||||| |||||
DB 29 GGGACGGCGGCTCGGTCAAT 10
||||| ||||| |||||

RESULT 6
AZ826864
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

AZ826864 31 bp DNA linear GSS 20-FEB-2001
2M0102H20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0102H20 R, genomic survey sequence.
AZ826864
AZ826864.1 GI:12996772
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 31)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D. Weiss R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: H column: 20
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers
1..31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

```

/db_xref="taxon:10090"
/clone="UUGC2M0102H20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb Purified UGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi14732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match      57.0%; Score 11.4; DB 9; Length 31;
Best Local Similarity 92.3%; Pred. No. 1.1e+06;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCT 13
|||||
Db 19 GGGACGGCGTCT 31

RESULT 7
AJ587908/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 339B10, genomic survey sequence.
AJ587908
VERSION
AJ587908.1 GI:37937532
KEYWORDS
GSS; left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
1
AUTHORS
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Leclercq, A.
TITLE
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL
EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED
12446565
REFERENCE
2 (bases 1 to 23)
AUTHORS
Balzerque, S.
TITLE
Direct Submission
JOURNAL
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
FEATURES
Location/Qualifiers

source
1..23
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_lib="339B10"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
misc_feature
1..23
/note="T-DNA flanking sequence
left border"

ORIGIN
Query Match      56.0%; Score 11.2; DB 10; Length 23;
Best Local Similarity 81.2%; Pred. No. 1.4e+06;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGG 16
|||||
Db 21 GGGACGCGCGCATGG 6

RESULT 8
CD028820
LOCUS
DEFINITION
grisea cDNA clone mgmy006x17 5', mRNA sequence.
CD028820
VERSION
CD028820.1 GI:30410276
KEYWORDS
EST.
SOURCE
Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

REFERENCE
1 (bases 1 to 31)
AUTHORS
Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Shatterai, K. and Dean, R.A.
TITLE
Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL
Unpublished (2002)
COMMENT
Contact: Ebbale DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgmy006 row: A column: 17
Seq primer: T3.
FEATURES
Location/Qualifiers

source
1..31
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgmy006x17"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea MY Uni-Zap XR Library"
/note="Vector: pBluescriptSK+; Site 1: EcoRI; Site 2: XhoI; Unidirectional cloning. EcoRI site has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Minimal medium mycelium library. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment. Otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

```

| | |
|-----------------------|--|
| | and selected for ampicillin resistance." |
| ORIGIN | |
| Query Match | 55.0%; Score 11; DB 9; Length 21; |
| Best Local Similarity | 100.0%; Pred. No. 1.7e+06; |
| Matches | 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY | 1 GGGACGCGGC 11 |
| Db | 16 GGGACGCGGC 6 |
| RESULT 10 | |
| AJ599957 | |
| LOCUS | Arabidopsis thaliana T-DNA flanking sequence, left border, clone |
| DEFINITION | 497C08 genomic survey sequence. |
| ACCESSION | AJ599957 |
| VERSION | AJ599957.1 GI:37949585 |
| KEYWORDS | GSS; left border; T-DNA flanking sequence. |
| SOURCE | Arabidopsis thaliana (thale cress) |
| ORGANISM | Arabidopsis thaliana |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi. |
| AUTHORS | Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepoint,E., Caboche,M. and Lecharny,A. T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites |
| TITLE | EMBO Rep. 3 (12), 1152-1157 (2002) |
| JOURNAL | PUBMED |
| REFERENCE | 12446565 |
| AUTHORS | 2 (bases 1 to 33) Balzergue,S. |
| JOURNAL | Direct Submission |
| COMMENT | Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.versailles.inra.fr/publiclines/ . This sequence has been generated in the framework of the French plant genomics program 'genoplante' (http://www.genoplante.com) and http://genoplante-info.infobiogen.fr . |
| FEATURES | Location/Qualifiers |
| source | 1..33 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /clone="497C08" /clone_lib="Arabidopsis thaliana T-DNA insertion lines" /ecotype="Wassilewskija" |
| misc_feature | 1..33 /note="T-DNA flanking sequence left border" |
| ORIGIN | |
| Query Match | 55.0%; Score 11; DB 10; Length 33; |
| Best Local Similarity | 100.0%; Pred. No. 1.6e+06; |
| Matches | 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY | 1 GGGACGCGGC 11 |
| Db | 23 GGGACGCGGC 33 |
| RESULT 11 | |
| AA259780/c | |

3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utm.utoronto.ca
Plate: UTM-UM-D126/7-061-UTM row: 08 column: D
Seq primer: T7 Reverse (5' GAGTAATACGACTACTATAGGG 3')
High quality sequence stop: 25.
Location/Qualifiers

FEATURES

source

1. .25
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="PBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/notes="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN

Query Match 53.0%; Score 10.6; DB 6; Length 25;
Best Local Similarity 76.5%; Pred. No. 2.5e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGGTC 18

Db 24 GGACGGCTGGTGCATC 8

RESULT 14

CF643257/c

LOCUS

DEFINITION D62_B05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

ACCESSION CF643257

VERSION CF643257.1 GI:37411392

KEYWORDS EST.

SOURCE Ustilago maydis

ORGANISM

Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

1 (bases 1 to 29)

Nugent, K.G., Choffe, K. and Saville, B.J.

Gene expression during Ustilago maydis diploid filamentous growth:

EST library creation and analyses

Fungal Genet. Biol. 41 (3), 349-360 (2004)

14761795

Contact: Barry J. Saville

Saville Lab

University of Toronto

3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada

Tel: 905 569 4702

Fax: 905 828 3792

Email: bsaville@utm.utoronto.ca

Plate: UTM-UM-D126/7-062-UTM row: 05 column: B

Seq primer: T7 Reverse (5' GAGTAATACGACTACTATAGGG 3')

High quality sequence stop: 29.

FEATURES

source

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/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="PBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/notes="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN

Query Match 53.0%; Score 10.6; DB 6; Length 29;
Best Local Similarity 76.5%; Pred. No. 2.5e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGGTC 18

Db 28 GGACGGCTGGTGCATC 12

RESULT 15

AG216212/c

LOCUS

DEFINITION Drosophila melanogaster DNA, clone:NP1197-5-1, flanking P[GawB] transposon insertion, genomic survey sequence.

ACCESSION AG216212

VERSION AG216212.1 GI:22763212

KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1

AUTHORS

Hayashi, S., Ito, K., Sado, Y., Taniguchi, M., Akimoto, A., Takeuchi, H., Aigaki, T., Matsuzaki, F., Nakagoshi, H., Tanimura, T., Ueda, R., Uemura, T., Yoshihara, M. and Goto, S.

GETDB, a database compiling expression patterns and molecular

locations of a collection of Gal4 enhancer traps

Genesis (2002) in press

2 (bases 1 to 33)

Hayashi, S.

Direct Submission

Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for

Developmental Biology, Laboratory for Morphogenetic Signaling;

Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan

(E-mail: shayashi@cdb.riken.go.jp, Tel: 81-78-301-3184,

Fax: 81-78-301-3183)

This clone was isolated from genomic DNA flanking an insertion of

the P element vector P[GawB] of a Drosophila strain.

FEATURES

source

1. .33 Location/Qualifiers

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/strain="NP1197"

/db_xref="taxon:7227"

/chromosome="2"

/map="54C6"

/clone="NP1197-5-1"

/note="flanking P[GawB] transposon insertion"

ORIGIN

Query Match 53.0%; Score 10.6; DB 10; Length 33;
Best Local Similarity 76.5%; Pred. No. 2.4e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGGTC 18

Db 22 GCACTGCTGCACGGTC 6

Search completed: November 27, 2005, 06:30:03

Job time : 3611 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 27, 2005, 04:52:55 ; Search time 135 Seconds
(without alignments)
263.342 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacgcccgcctcgatc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1065270

Minimum DB seq length: 12

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 14.2 | 71.0 | 33 | 3 | US-09-977-137A-16 |
| C 2 | 14 | 70.0 | 25 | 3 | US-09-396-196G-42173 |
| C 3 | 13.8 | 69.0 | 25 | 3 | US-09-396-196G-46323 |
| C 4 | 13.8 | 69.0 | 25 | 3 | US-09-396-196G-46324 |
| C 5 | 13.8 | 69.0 | 25 | 3 | US-09-396-196G-46335 |
| C 6 | 13.2 | 66.0 | 25 | 3 | US-09-396-196G-53301 |
| 7 | 13 | 65.0 | 20 | 3 | US-09-046-858A-19 |
| 8 | 13 | 65.0 | 20 | 3 | US-09-450-515-19 |
| 9 | 13 | 65.0 | 20 | 3 | US-10-206-654-19 |
| 10 | 12.6 | 63.0 | 20 | 3 | US-10-131-827-8773 |
| C 11 | 12.6 | 63.0 | 24 | 3 | US-09-540-014-35 |
| C 12 | 12.6 | 63.0 | 24 | 3 | US-09-164-210-12 |
| C 13 | 12.6 | 63.0 | 24 | 3 | US-09-538-864-14 |
| C 14 | 12.6 | 63.0 | 24 | 3 | US-10-091-841A-35 |
| C 15 | 12.6 | 63.0 | 25 | 3 | US-09-396-196G-40648 |
| C 16 | 12.6 | 63.0 | 30 | 3 | US-09-319-648-52 |
| 17 | 12.6 | 63.0 | 30 | 9 | 5240848-8 |
| 18 | 12.4 | 62.0 | 20 | 2 | US-08-182-175A-9 |
| C 19 | 12.4 | 62.0 | 20 | 2 | US-08-474-633A-16 |
| C 20 | 12.4 | 62.0 | 20 | 3 | US-08-823-771-16 |
| 21 | 12.4 | 62.0 | 20 | 6 | PCT-US92-06412-9 |
| C 22 | 12.4 | 62.0 | 25 | 3 | US-09-396-196G-41065 |
| C 23 | 12.4 | 62.0 | 25 | 3 | US-09-396-196G-46162 |
| C 24 | 12.4 | 62.0 | 25 | 3 | US-09-396-196G-46163 |

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|------|------|------|----|---|----------------------|-------------------|
| 25 | 12.2 | 61.0 | 21 | 3 | US-09-158-863C-38 | Sequence 38, Appl |
| C 26 | 12.2 | 61.0 | 22 | 3 | US-09-589-560B-58 | Sequence 58, Appl |
| C 27 | 12.2 | 61.0 | 22 | 3 | US-09-589-560B-62 | Sequence 62, Appl |
| C 28 | 12.2 | 61.0 | 25 | 3 | US-09-396-196G-25195 | Sequence 25195, A |
| C 29 | 12.2 | 61.0 | 25 | 3 | US-09-396-196G-49392 | Sequence 49392, A |
| C 30 | 12.2 | 61.0 | 34 | 3 | US-09-487-558B-3 | Sequence 2, Appl |
| C 31 | 12 | 60.0 | 23 | 3 | US-09-462-671-1 | Sequence 1, Appl |
| C 32 | 12 | 60.0 | 27 | 3 | US-08-485-355B-4 | Sequence 4, Appl |
| C 33 | 12 | 60.0 | 29 | 3 | US-09-045-583-45 | Sequence 45, Appl |
| C 34 | 12 | 60.0 | 29 | 3 | US-09-534-185-45 | Sequence 45, Appl |
| C 35 | 12 | 60.0 | 32 | 3 | US-08-485-355B-30 | Sequence 30, Appl |
| C 36 | 12 | 60.0 | 32 | 3 | US-09-045-583-44 | Sequence 44, Appl |
| C 37 | 12 | 60.0 | 32 | 3 | US-09-534-185-44 | Sequence 44, Appl |
| C 38 | 11.8 | 59.0 | 17 | 2 | US-08-171-299B-6 | Sequence 6, Appl |
| C 39 | 11.8 | 59.0 | 20 | 3 | US-09-467-642-13 | Sequence 13, Appl |
| C 40 | 11.8 | 59.0 | 23 | 3 | US-08-930-797B-2 | Sequence 2, Appl |
| C 41 | 11.8 | 59.0 | 27 | 2 | US-08-580-401-5 | Sequence 5, Appl |
| C 42 | 11.8 | 59.0 | 27 | 2 | US-08-927-394-8 | Sequence 8, Appl |
| C 43 | 11.8 | 59.0 | 31 | 2 | US-08-927-394-7 | Sequence 7, Appl |
| C 44 | 11.6 | 58.0 | 18 | 3 | US-09-402-618B-75 | Sequence 75, Appl |
| C 45 | 11.6 | 58.0 | 18 | 3 | US-09-942-588A-31 | Sequence 31, Appl |

ALIGNMENTS

RESULT 1
US-09-977-137A-16
; Sequence 16, Application US/09977137A
; Patent No. 6750042
; GENERAL INFORMATION:
; APPLICANT: Summers, Anne O.
; TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 79-00
; CURRENT APPLICATION NUMBER: US/09/977,137A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,465
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-977-137A-16

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| Qy | 1 | GGACGCGGCTCGGTCA 19 | Query Match | 71.0%; | Score 14.2; | DB 3; | Length 33; |
| Db | 6 | GGGTCTCGGCTCGGCA 24 | Best Local Similarity | 84.2%; | Pred. No. 3e+03; | Mismatches 0; | Gaps 0; |
| | | | Matches 16; | Conservative 0; | Indels 3; | | |

RESULT 2
US-09-396-196G-42173/c
; Sequence 42173, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678

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; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42173
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-42173

Query Match      70.0%; Score 14; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CGGCGCTCGGTTCAT 20
Db 20 CGGCGCTCGGTTCAT 7

RESULT 3
US-09-396-196G-46323/c
; Sequence 46323, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46323
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46323

Query Match      69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
Db 20 ACGCTGCGCACGGTTCAT 4

RESULT 4
US-09-396-196G-46324/c
; Sequence 46324, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46324
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46324

Query Match      69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
Db 20 ACGCTGCGCACGGTTCAT 4

RESULT 5
US-09-396-196G-46335/c
; Sequence 46335, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46335
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46335

Query Match      69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACGCGCGCTCGGTTCAT 20
Db 18 ACGCTGCGCACGGTTCAT 2

RESULT 6
US-09-396-196G-53301
; Sequence 53301, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53301
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-53301

Query Match      66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GACGCGCGCTCGGTTCAT 20
Db 2 GACCCAGCGCTCTGTTCAT 19
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```
RESULT 7
US-09-046-858A-19
; Sequence 19, Application US/09046858A
; Patent No. 6048973
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-450-515-19
Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGCGGCGCTCG 15
Db 2 GACGCGGCGCTCG 14

RESULT 9
US-10-206-654-19
; Sequence 19, Application US/10206654
; Patent No. 6919493
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/206,654
; FILING DATE: 25-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:

QY 3 GACGCGGCGCTCG 15
Db 2 GACGCGGCGCTCG 14

RESULT 8
US-09-450-515-19
; Sequence 19, Application US/09450515
; Patent No. 6680425
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-046-858A-19
Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGCGGCGCTCG 15
Db 2 GACGCGGCGCTCG 14

RESULT 8
US-09-450-515-19
; Sequence 19, Application US/09450515
; Patent No. 6680425
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/042,376
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-206-654-19

Query Match          65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGCGCGCTCG 15
   |||||
Db 2 GACGCGCGCTCG 14

RESULT 10
US-10-131-827-8773
; Sequence 8773, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8773
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human cytomegalovirus
US-10-131-827-8773

Query Match          63.0%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGCGCGCTCGGTTCAT 20
   |||||
Db 1 GTACGCGCTCGTGGTTCAT 19

RESULT 11
US-09-540-014-35/c
; Sequence 35, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21

; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-206-654-19

Query Match          65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGCGCGCTCG 15
   |||||
Db 2 GACGCGCGCTCG 14

RESULT 10
US-10-131-827-8773
; Sequence 8773, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8773
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human cytomegalovirus
US-10-131-827-8773

Query Match          63.0%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGCGCGCTCGGTTCAT 20
   |||||
Db 1 GTACGCGCTCGTGGTTCAT 19

RESULT 11
US-09-540-014-35/c
; Sequence 35, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21

; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-206-654-19

Query Match          65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGCGCGCTCG 15
   |||||
Db 2 GACGCGCGCTCG 14

RESULT 10
US-10-131-827-8773
; Sequence 8773, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8773
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human cytomegalovirus
US-10-131-827-8773

Query Match          63.0%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGCGCGCTCGGTTCAT 20
   |||||
Db 1 GTACGCGCTCGTGGTTCAT 19

RESULT 11
US-09-538-864-14/c
; Sequence 14, Application US/09538864
; Patent No. 6784346
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; APPLICANT: Wong, Joshua
; APPLICANT: Marx, Corina
; TITLE OF INVENTION: Value-Added Traits in Grain and Seed
; TITLE OF INVENTION: Transformed with Thioredoxin
; FILE REFERENCE: 2001-0703.30
; CURRENT APPLICATION NUMBER: US/09/538,864
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/126,736
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
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; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-538-864-14

Query Match 63.0%; Score 12.6; DB 3; Length 24;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCGCTCGGTCAAT 20
Db 19 GCACGAGCGCTCGGATAT 1

RESULT 14
US-10-091-841A-35/c
; Sequence 35, Application US/10091841A
; Patent No. 6833493
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Gel Val, Gregorio
; APPLICANT: Calliau, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: BARLEY GENE FOR THIOREDOXIN AND
; TITLE OF INVENTION: NADP-THIOREDOXIN REDUCTASE
; FILE REFERENCE: 416272001410
; CURRENT APPLICATION NUMBER: US/10/091.841A
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-091-841A-35

Query Match 63.0%; Score 12.6; DB 3; Length 24;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCGCTCGGTCAAT 20
Db 19 GCACGAGCGCTCGGATAT 1

RESULT 15
US-09-396-196G-40648/c
; Sequence 40648, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann

; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40648
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-40648

Query Match 63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCGCTCGGTCAAT 20
Db 25 GCACGGCGCGATCGATCAT 7

Search completed: November 27, 2005, 06:32:29
Job time : 135 secs

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| Result No. | Score | Query | | Length | DB | ID | Description |
|------------|-------|-------|------|--------|----------------------|----------------------|--------------------|
| | | Match | % | | | | |
| 1 | 20 | 100.0 | 20 | 7 | US-10-605-498-82 | | Sequence 82, Appl |
| | 20 | 100.0 | 21 | 7 | US-10-605-498-81 | | Sequence 81, Appl |
| c 2 | 19 | 95.0 | 19 | 7 | US-10-605-498-90 | | Sequence 90, Appl |
| | 4 | 16 | 80.0 | 21 | 7 | US-10-605-498-3 | |
| c 5 | 15 | 76.0 | 25 | 7 | US-10-719-956-135321 | | Sequence 135321 |
| | 6 | 15 | 75.0 | 21 | 7 | US-10-605-498-4 | |
| 7 | 14.2 | 71.0 | 25 | 10 | US-11-036-317-261850 | | Sequence 261850, |
| | 8 | 14.2 | 71.0 | 25 | 10 | US-11-036-317-269817 | |
| 9 | 14.2 | 71.0 | 25 | 10 | US-11-036-317-330516 | | Sequence 330516, |
| | 10 | 14.2 | 71.0 | 25 | 10 | US-11-036-317-332488 | |
| 11 | 14.2 | 71.0 | 25 | 10 | US-11-036-317-364485 | | Sequence 364485, |
| | 12 | 14.2 | 71.0 | 25 | 10 | US-11-036-317-406575 | |
| 13 | 14.2 | 71.0 | 25 | 10 | US-11-036-317-536426 | | Sequence 536426, |
| | 14 | 14.2 | 71.0 | 25 | 10 | US-11-036-317-536427 | |
| 15 | 14.2 | 71.0 | 33 | 3 | US-09-977-137A-16 | | Sequence 16, Appl |
| 16 | 14 | 70.0 | 25 | 5 | US-10-215-112-7242 | | Sequence 7242, App |
| | 17 | 14 | 70.0 | 25 | 9 | US-10-809-189-42173 | |
| c 18 | 13.8 | 69.0 | 25 | 9 | US-10-809-189-46323 | | Sequence 46323, A |
| | 19 | 13.8 | 69.0 | 25 | 9 | US-10-809-189-46324 | |
| c 20 | 13.8 | 69.0 | 25 | 9 | US-10-809-189-46335 | | Sequence 46335, A |
| | 21 | 13.6 | 68.0 | 25 | 7 | US-10-719-956-135322 | |
| c 22 | 13.6 | 68.0 | 25 | 7 | US-10-719-956-198103 | | Sequence 198103, |
| | 23 | 13.6 | 68.0 | 25 | 8 | US-10-719-900-309243 | |

; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-81

Query Match 100.0%; Score 20; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.5; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGGACGGCGCTCGGTGCAT 20
Db 2 GGGACGGCGCTCGGTGCAT 21
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RESULT 3

US-10-605-498-90/c
; Sequence 90, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-605-498-90

Query Match 95.0%; Score 19; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGACGGCGCTCGGTGCAT 20
Db 19 GGGACGGCGCTCGGTGCAT 1
|||||

RESULT 4

US-10-605-498-3
; Sequence 3, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18

; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-3

Query Match 80.0%; Score 16; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.9e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

Qy 5 CGCGCGCTCGGTGCAT 20
Db 1 CGCGCGCTCGGTGCAT 16
|||||

RESULT 5

US-10-719-956-135321/c
; Sequence 135321, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 135321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-135321

Query Match 76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTGCAT 20
Db 25 GGGACGAACGCTCGGCCAT 6
|||||

RESULT 6

US-10-605-498-4
; Sequence 4, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-4

Query Match 75.0%; Score 15; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGCTCG 15
    |||||
Db 7 GGGACGGCGCTCG 21

RESULT 7
US-11-036-317-261850
; Sequence 261850, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 261850
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-261850

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGCTCGGTCA 19
    |||||
Db 3 GGGACGGCGGTGCA 21

RESULT 8
US-11-036-317-269817
; Sequence 269817, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 269817
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-269817

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGCTCGGTCA 19
    |||||
Db 5 GGGACGGCGGTGCA 23

RESULT 9
US-11-036-317-330516
; Sequence 330516, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
```

```
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 330516
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-330516

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGCTCGGTCA 19
    |||||
Db 1 GGGACGGCGGTGCA 19

RESULT 10
US-11-036-317-332488
; Sequence 332488, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 332488
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-332488

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGCTCGGTCA 19
    |||||
Db 2 GGGACGGCGGTGCA 20

RESULT 11
US-11-036-317-364465
; Sequence 364465, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 364465
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
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US-11-036-317-364465

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGCGCTCGGTCA 19
| | | | | | | | | | | | | | | | | | | | |
Db 4 GGGACGCGCGCATCTGCCA 22

RESULT 12

US-11-036-317-406575
; Sequence 406575, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 406575
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-406575

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGCGCTCGGTCA 19
| | | | | | | | | | | | | | | | | | | | |
Db 7 GGGACGAGCGCTTTGTCA 25

RESULT 13

US-11-036-317-536426
; Sequence 536426, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 536426
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-536426

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGCGCTCGGTCA 19
| | | | | | | | | | | | | | | | | | | | |
Db 7 GGGACGAGCGCTTTGTCA 25

RESULT 14

US-11-036-317-536427

; Sequence 536427, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 536427
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-536427

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGCGCTCGGTCA 19
| | | | | | | | | | | | | | | | | | | | |
Db 7 GGGACGTGGCGCTTTGTCA 25

RESULT 15

US-09-977-137A-16
; Sequence 16, Application US/09977137A
; Publication No. US20030104524A1
; GENERAL INFORMATION:
; APPLICANT: Summers, Anne O.
; APPLICANT: Caguiat, Jonathan
; TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 79-00
; CURRENT APPLICATION NUMBER: US/09/977,137A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,465
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-977-137A-16

Query Match 71.0%; Score 14.2; DB 3; Length 33;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGCGCTCGGTCA 19
| | | | | | | | | | | | | | | | | | | | |
Db 6 GGTCTCGGCGCTCGGGCA 24

Search completed: November 27, 2005, 06:46:02
Job time : 798 secs

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OM nucleic - nucleic search, using sw model

Run on: November 27, 2005, 04:57:00 ; Search time 225 Seconds
(without alignments)
13.210 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacgcggcgctcggtcat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3205263 seqs, 74304013 residues

Total number of hits satisfying chosen parameters: 6389384

Minimum DB seq length: 12

Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.New.*

1: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------------------------|-------------------|
| C 1 | 12.8 | 64.0 | 19 | 8 US-11-101-244-1008030 | Sequence 1008030, |
| C 2 | 12.8 | 64.0 | 19 | 9 US-11-083-784-1008030 | Sequence 1008030, |
| C 3 | 12.6 | 63.0 | 19 | 8 US-11-101-244-899787 | Sequence 899787, |
| C 4 | 12.6 | 63.0 | 19 | 9 US-11-083-784-899787 | Sequence 899787, |
| C 5 | 12.2 | 61.0 | 22 | 7 US-11-176-795-58 | Sequence 58, Appl |
| C 6 | 12.2 | 61.0 | 22 | 7 US-11-176-795-58 | Sequence 877585, |
| C 7 | 12 | 60.0 | 19 | 8 US-11-101-244-877585 | Sequence 877585, |
| C 8 | 12 | 60.0 | 19 | 9 US-11-083-784-877585 | Sequence 877585, |
| C 9 | 11.8 | 59.0 | 19 | 8 US-11-101-244-367704 | Sequence 367704, |
| C 10 | 11.8 | 59.0 | 19 | 8 US-11-101-244-367714 | Sequence 367714, |
| C 11 | 11.8 | 59.0 | 19 | 8 US-11-101-244-385820 | Sequence 385820, |
| C 12 | 11.8 | 59.0 | 19 | 8 US-11-101-244-475963 | Sequence 475963, |
| C 13 | 11.8 | 59.0 | 19 | 8 US-11-101-244-1128971 | Sequence 1128971, |
| C 14 | 11.8 | 59.0 | 19 | 8 US-11-101-244-1221629 | Sequence 1221629, |
| C 15 | 11.8 | 59.0 | 19 | 9 US-11-083-784-367704 | Sequence 367704, |
| C 16 | 11.8 | 59.0 | 19 | 9 US-11-083-784-367714 | Sequence 367714, |
| C 17 | 11.8 | 59.0 | 19 | 9 US-11-083-784-385820 | Sequence 385820, |
| C 18 | 11.8 | 59.0 | 19 | 9 US-11-083-784-475963 | Sequence 475963, |
| C 19 | 11.8 | 59.0 | 19 | 9 US-11-083-784-1128971 | Sequence 1128971, |
| C 20 | 11.8 | 59.0 | 19 | 9 US-11-083-784-1221629 | Sequence 1221629, |
| C 21 | 11.6 | 58.0 | 19 | 8 US-11-101-244-992967 | Sequence 992967, |
| C 22 | 11.6 | 58.0 | 19 | 8 US-11-101-244-1512341 | Sequence 1512341, |
| C 23 | 11.6 | 58.0 | 19 | 8 US-11-101-244-1562938 | Sequence 1562938, |

ALIGNMENTS

RESULT 1

US-11-101-244-1008030/c
; Sequence 1008030, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1008030
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1008030

Query Match 64.0%; Score 12.8; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GACGCGCGCTCGGTC 18

Db 17 GATGAGCGCTCGGTC 2

RESULT 2

US-11-083-784-1008030/c
; Sequence 1008030, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1008030
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1008030

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GACGCGCGCTCGGTC 18
||| |||||
Db 17 GATGAGCGCTCGGTC 2

RESULT 3

US-11-101-244-899787
; Sequence 899787, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaco, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 899787
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-899787

Query Match 63.0%; Score 12.6; DB 8; Length 19;
Best Local Similarity 63.2%; Pred. No. 1.7e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGGTCAT 20
||| |||||
Db 1 GGAACGGCGCGGUUCAU 19

RESULT 4

US-11-083-784-899787
; Sequence 899787, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaco, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 899787
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-899787

Query Match 63.0%; Score 12.6; DB 9; Length 19;
Best Local Similarity 63.2%; Pred. No. 1.7e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGGTCAT 20
||| |||||
Db 1 GGAACGGCGCGGUUCAU 19

RESULT 5

US-11-176-795-58/c
; Sequence 58, Application US/11176795
; Publication No. US20050255517A1
; GENERAL INFORMATION:
; APPLICANT: Gerdes, John C
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 58
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Coliform Bacteria
US-11-176-795-58

Query Match 61.0%; Score 12.2; DB 7; Length 22;
Best Local Similarity 82.4%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGACGGCGCTCGGTC 18
||| |||||
Db 19 GGATGGCGCTCGGTC 3

RESULT 6

US-11-176-795-62/c
; Sequence 62, Application US/11176795
; Publication No. US20050255517A1
; GENERAL INFORMATION:
; APPLICANT: Gerdes, John C
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 62
; LENGTH: 22
; TYPE: DNA

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; ORGANISM: Coliform Bacteria
US-11-176-795-62

Query Match      61.0%; Score 12.2; DB 7; Length 22;
Best Local Similarity 82.4%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2 GGACGGCGCGCTCGGTC 18
    ||| ||||| |||||
Db   19 GGATGCGCGCTCGGTC  3

RESULT 7
US-11-101-244-877585/c
; Sequence 877585, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 877585
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-877585

Query Match      60.0%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 GCGCTCGGTCAT 20
    ||| ||||| |||||
Db   15 GCGCTCGGTCAT  4

RESULT 8
US-11-083-784-877585/c
; Sequence 877585, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 877585
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-877585/c

Query Match      59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  4 ACACGGCGCTCGGTC 18
    ||| ||||| |||||
Db   16 ACACGGCGCTCGGTC  2

RESULT 9
US-11-101-244-367704/c
; Sequence 367704, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 367704
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-367704

Query Match      59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  4 ACACGGCGCTCGGTC 18
    ||| ||||| |||||
Db   16 ACACGGCGCTCGGTC  2

RESULT 10
US-11-101-244-367714/c
; Sequence 367714, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 367714
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-367714
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; ORGANISM: Homo sapiens
US-11-101-244-367714

Query Match          59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  ACGCGCGCTCGGTC 18
         ||| ||||| |||||
Db       15  ACACGGCGCTTGGTC 1

RESULT 11
US-11-101-244-385820/c
; Sequence 385820, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 385820
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-385820

Query Match          59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3  GACGCGCGCTCGGT 17
         ||| ||||| |||||
Db       17  GAGGTGGCGCTCGGT 3

RESULT 12
US-11-101-244-475963
; Sequence 475963, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 475963
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-475963

Query Match          59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  ACGCGCGCTCGGTC 18
         ||| ||||| |||||
Db       17  ACGCGGTGCTTGGTC 3

RESULT 13
US-11-101-244-1128971/c
; Sequence 1128971, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1128971
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1128971

Query Match          59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  ACGCGCGCTCGGTC 18
         ||| ||||| |||||
Db       17  ACGCGGTGCTTGGTC 3

RESULT 14
US-11-101-244-1221629/c
; Sequence 1221629, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1221629
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1221629
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Query Match 59.0%; Score 11.8; DB 8; Length 19;
 Best Local Similarity 86.7%; Pred. No. 3.6e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGGCGCTCGGTC 18
 Db 16 ACGTGAGCTCGGTC 2

RESULT 15

US-11-083-784-367704/c
 ; Sequence 367704, Application US/11083784
 ; Publication No. US20050245475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 1349US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR APPLICATION NUMBER: US/10/714,333
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 367704
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; US-11-083-784-367704

Query Match 59.0%; Score 11.8; DB 9; Length 19;
 Best Local Similarity 86.7%; Pred. No. 3.6e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGGCGCTCGGTC 18
 Db 16 ACACGGCGCTTGTC 2

Search completed: November 27, 2005, 06:50:00
 Job time : 226 secs

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